

## Supplementary Information

**Figure S1.** Open reading frame and amino acid sequence of the *GhLRP* gene. (A) Open reading frame sequence of the *GhLRP* gene; (B) GhLRP protein sequence; (C) Amino acid composition of the GhLRP protein.

(A)

1	ATGATCGGTA GCCCACCCGT CTCGTCAACG ACTCGACATT TATTCCAGAC ACAAAACAACC
61	TCATCAGAGC TGCCACAATT GGCTTCAAAA TACAAAAAAGC ACGAAGAGTC TGAATACAAA
121	CAGCCAAAAT ATCACGAAGA GCACCCAAAA CATGAGAAGC CTGAAATGCA CAAGGAGGAA
181	AGACAAAAAAC CCTACAAACA ACATGAAGAG TACCACGAGT CACACGAATC GAAGAAGCAC
241	GAAGAGTACA ATAAAGACAA ACCCGATTTC CCCAAATGGG AAAAGCCTAA AGAGCACGAG
301	AAACACGAAG TCGAATATCC GAAAATACCC GAGTACAAGG ACAAAACAAGA TGAGGATAAG
361	GAACATAAAA ATGAAGAGTT CCACGAATCA CGCGAATCAA AGGAGCACAA AGAGTATGAG
421	AAAGAAAAAAC CCGAGTCCCC CAAACAGCAA AAGCCTAAAG AGCACGAGAA ACACCAAGTC
481	GAATATCCGG AAATAACCCA GTACAAGGAA GAGCAAGATA AGAGTAAGGA ACATAAAAGAT
541	GAAGAGTGCC ACGAGTCACA CGAATCGAAA GAGCACGAAG AGTACTAG

(B)

1	MIGSHTVSST TRHLFQTQTT
21	SSELPQLASK YKKHEESEYK
41	QPKYHEEHPK HEKPEMHKEE
61	RQKPYKQHEE YHESHESKKH
81	EEYNKDKPDF PKWEKPKEHE
101	KHEVEYPKIP EYKDKQDEDK
121	EHKNEEFHES RESKEHKEYE
141	KEKPEFPKQQ KPKEHEKHQV
161	EYPEITQYKE EQDKSKEHKD
181	EECHESHESK EHEEY*

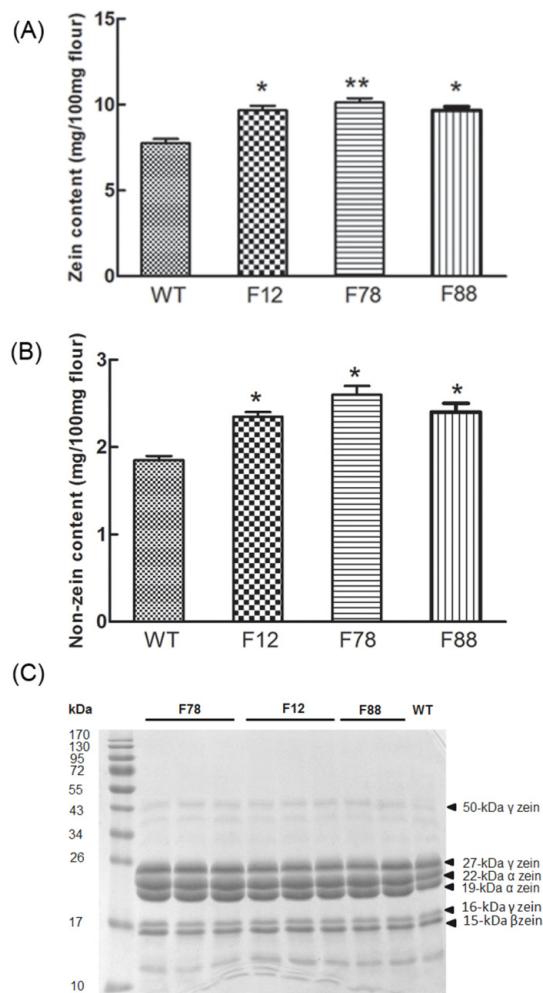
(C)

Amino acid	Num	%w/w
A Ala	1	0.32
C Cys	1	0.44
D Asp	7	3.36
E Glu	47	24.93
F Phe	4	2.38
G Gly	1	0.27
H His	22	12.30
I Ile	3	1.42
K Lys	36	18.97
L Leu	3	1.42
M MET	2	1.08
N Asn	2	0.95
P Pro	14	5.81
Q Gln	12	6.32
R Arg	3	1.88
S Ser	14	5.30
T Thr	7	3.01
V Val	3	1.27
W Trp	1	0.74
Y Tyr	12	7.84

**Figure S2.** Selection of maize resistant callus and plant regeneration. **(A)** Maize callus on selection medium containing 15 mg/L hygromycin; **(B)** Differentiation of resistant callus; **(C)** Regenerated plants in the rooting medium; **(D)** Regenerated plants in a flowerpot; **(E)** Regenerated plants in the field; **(F)** T<sub>0</sub> transgenic maize seeds.



**Figure S3.** Zein and non-zein accumulation pattern in T<sub>4</sub> kernels of three transgenic lines. (A) Zein content; (B) Non-zein content. All the calculations were performed with technical triplicates and biological triplicates, and 20 mature kernels were used per assay. Student's *t*-test is used to evaluate the difference between the transgenic maize and WT (\*  $p < 0.05$ ; \*\*  $p < 0.01$ ); (C) Zein proteins of WT, F12, F78, and F88 lines were analyzed by SDS-PAGE. For SDS-PAGE, 5  $\mu$ L samples were loaded to 15% polyacrylamide gel. The size for each protein marker and sample band was indicated by the numbers in the “kDa” columns.



**Table S1.** Agronomic traits of T<sub>3</sub> kernels in three transgenic lines.

Line	PH (cm)	EH (cm)	EL (cm)	BTL (cm)	ED (cm)	ER	KW (g)
F12	200.7 ± 3.2	98.7 ± 5.4	11.8 ± 1.8	1.0 ± 0.7	37.7 ± 0.8	14	24.4 ± 0.9
F78	198.5 ± 7.5	89.3 ± 5.8	13.2 ± 1.6	0.4 ± 0.3	42.7 ± 1.2	16	25.2 ± 1.2
F88	210.3 ± 4.2	92.3 ± 4.2	12.0 ± 1.3	1.9 ± 1.4	39.2 ± 2.8	14	27.3 ± 3.4
WT <sup>a</sup>	202.5 ± 5.8	89.3 ± 3.8	11.3 ± 2.3	0.7 ± 0.6	39.8 ± 0.3	16	26.8 ± 4.0

<sup>a</sup> The segregating populations of hybrid 08 × 178 in T<sub>3</sub> were used as a control (WT). PH, plant height; EH, ear height; EL, ear length; BTL, bald tip length; ED, ear diameter; ER, number of ear rows; KW, 100-kernel weight. Values are average measurements for each line in T<sub>2</sub> progenies ± standard deviation. Differences in agronomic traits between transgenic lines and WT were analyzed using a Student's *t*-test.